

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds

(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-2

Sequence: 578 1 QDWLTFQKXHLNTRVDNCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: ELOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_todent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_virus:\*  
16: SP\_Dactylap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	127	13	Q918V8
2	556	96.2	127	13	Q8UVX5
3	404.5	70.0	129	13	Q9DFY6
4	386	66.8	128	13	Q9DFY8
5	311	53.8	128	13	Q9DFY7
6	309	53.5	128	13	Q9DFY5
7	298	51.6	133	13	Q98SM0
8	286	49.5	133	13	Q98SM1
9	285	49.3	132	13	Q98SM2
10	282	48.4	132	13	Q98SM1
11	280	47.7	132	13	Q98SM1
12	275.5	47.7	132	13	Q9DFY8
13	157.5	27.2	169	13	Q9DFY8
14	129.5	22.4	146	6	Q861Y3
15	129.5	22.4	146	6	Q861Y2
16	129.5	22.4	146	6	Q861Y1

17	129	22.3	152	11	Q9UKI5	Q9UKI5 mus saxicol
18	127	22.0	157	11	Q9UKI9	Q9UKI9 meriones un
19	126.5	21.9	153	11	Q9UKI7	Q9UKI7 mus saxicol
20	126	21.8	157	11	Q9UKI3	Q9UKI3 meriones un
21	125.5	21.7	146	6	Q861Y4	Q861Y4 trachypithe
22	125	21.6	157	11	Q9UKJ4	Q9UKJ4 meriones un
23	123	21.3	154	11	Q9UKI8	Q9UKI8 meriones un
24	122	21.1	157	11	Q9UKJ1	Q9UKJ1 mus saxicol
25	122	20.9	147	6	Q7YRJ6	Q7YRJ6 dalaena mys
26	121	20.9	157	11	Q9UKJ2	Q9UKJ2 meriones un
27	120.5	20.8	155	11	Q9UKJ3	Q9UKJ3 mus saxicol
28	119.5	20.7	155	11	Q9UKJ9	Q9UKJ9 meriones un
29	118	20.4	147	6	Q7YRJ5	Q7YRJ5 mus pahari
30	116.5	20.2	155	11	Q9UKI6	Q9UKI6 mus saxicol
31	115.5	20.0	132	6	Q9TVJ25	Q9TVJ25 eulemur ful
32	115.5	20.0	155	11	Q9UKI2	Q9UKI2 mus saxicol
33	115.5	20.0	155	11	Q9UKI4	Q9UKI4 mus saxicol
34	115	19.9	146	6	Q861Y5	Q861Y5 colobus que
35	114.5	19.8	170	6	Q9BRC1	Q9BRC1 tragulus ja
36	113.5	19.6	119	6	Q9TSO6	Q9TSO6 cercopithe
37	113.5	19.6	119	6	Q9TVJ32	Q9TVJ32 gorilla gor
38	113.5	19.6	132	6	Q9TVJ24	Q9TVJ24 galago moho
39	113.5	19.6	147	6	Q8HZQ0	Q8HZQ0 pan troglod
40	113.5	19.6	155	11	Q9UKI34	Q9UKI34 rattus norv
41	113	19.6	156	11	Q9UKG6	Q9UKG6 mus caroli
42	113	19.6	156	11	Q9UKH7	Q9UKH7 mus caroli
43	112.5	19.5	119	6	Q9TVJ30	Q9TVJ30 saginus oe
44	112.5	19.5	155	11	Q9UKI25	Q9UKI25 mus musculu
45	112.5	19.5	155	11	Q9UKH8	Q9UKH8 mus pahari

## ALIGNMENTS

## RESULT 1

ID Q918V8 PRELIMINARY; PRT; 127 AA.

AC Q918V8; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

OS Onconase variant rap1 precursor.

OC Rana pipiens (Northern leopard frog).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

NCBI\_TaxID=8404;

[1] SEQUENCE FROM N.A.

RP TISSUE=Liver;

RX MEDLINE=20330357; PubMed=10871370;

RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;

RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a

Nucleic Acids Res. 28:2375-2382(2000)."

RL EMBL: A165133; AAT76935.1; -.

DR PTR: A39035; A39035.

DR HSBP; P22069; IONC.

DR GO: GO:0003676; F:nucleic acid binding; IEA.

DR GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro: IPR001427; RNAseA.

DR Pfam: PF00074; RNAseA; 1.

DR PRODOM: PD000535; RNAseA; 1.

DR SMART: SM00092; RNAse\_Pc; 1.

DR PROSITE: PS00127; RNAse\_PANCREATIC; 1.

KW SIGNAL.

FT SIGNAL.

SO SEQUENCE

1 23 POTENTIAL.

127 AA; 14491 MW; B8511DC5407AB59B CRC64;

Query Match 100.0%; Score 578; DB 13; Length 127;

Best Local Similarity 100.0%; Pred. No. 3.5e-59;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLNTRVDNCNIMSTVLHFCKDKNRTFYRPEPVKAICGIIASKNVLT 60

Db 24 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 83  
 QY 61 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 104  
 Db 84 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 127

## RESULT 2

Q8UVX5 PRELIMINARY; PRT; 127 AA.  
 AC Q8UVX5;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Oncocase precursor.  
 GN RPR.  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 NCBI\_TaxID=8404;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Liao Y.-D., Wang S.-C.;  
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF332139; AAL54383.1; -.  
 DR PIR; A39035; A39035.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA. 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 DR Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 127 AA; 14469 MW; 953F90B351CFEFP3 CRC64;

Query Match 96.2%; Score 556; DB 13; Length 127;  
 Best Local Similarity 96.2%; Pred. No. 1.2e-56;  
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 60  
 Db 24 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 83  
 QY 61 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 104  
 Db 84 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 127

## RESULT 3

Q9DFY6 PRELIMINARY; PRT; 129 AA.  
 AC Q9DFY6;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE RC-RNase4 ribonuclease precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Tissue=Liver;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.W., Tang P.C., Wang S.C.;  
 RT "Purification and cloning of cytotolic ribonucleases from Rana  
 catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104(2000).  
 RN (2)

QY 1 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 60  
 Db 24 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 83  
 QY 61 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 104  
 Db 84 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 127

RP SEQUENCE FROM N.A.  
 RC Tissue=Liver;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF242555; AAG31441.2; -.  
 DR PDB; 1KVZ; 28-JUL-02.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 DR Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 70.0%; Score 404.5; DB 13; Length 129;  
 Best Local Similarity 67.6%; Pred. No. 4.6e-39;  
 Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 1 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 60  
 Db 24 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 83  
 QY 61 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 104  
 Db 84 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 127

## RESULT 4

Q9DFY8 PRELIMINARY; PRT; 128 AA.  
 AC Q9DFY8;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE RC-RNase2 ribonuclease precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Tissue=Liver;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.W., Tang P.C., Wang S.C.;  
 RT "Purification and cloning of cytotolic ribonucleases from Rana  
 catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104(2000).  
 RN (2)

RP SEQUENCE FROM N.A.  
 RC Tissue=Liver;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF242553; AAG31439.1; -.  
 DR PDB; 1M58; 09-JUN-03.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 DR Signal.  
 FT SIGNAL.  
 SQ CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.  
 SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;  
 Best Local Similarity 67.3%; Pred. No. 6.4e-37;  
 Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 60  
 Db 24 QDWLTFQKHLTNTDVPDCCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIITASKNVLTT 83  
 QY 61 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 104  
 Db 84 SEFYISDCNVTSPCKYKTKKSTNTFCVTCENQAPVHFGVGHG 127